FIG. 1

FIG. 2

FIG. 3

Fig. 4A

(1 Light chain amino acid sequence:

1
LLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPTTFGGGTKLEIKRADAAPTVSIFPPSSE

2
TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

3

(1 Heavy Chain amino acid sequence:

4
/QLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDYAHAMDYWGQGTSVTVSSAKTTA

5
SVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPD

6
KDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEMTKKQVTLTCM

TDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHttKSFSRTPG

(1 heavy chain nucleotide sequence:

:gggttggtcctgtatcatcctattcctgtggtgccactgccacagtgtgcactccgacgtgcagctcaggagtcaggacctgt
:tgtcactgactactccatcaccagtgattacgcctggaactggatacggcaattcccaggtaacaagctggagtgagtggatgggctacatat
:caaagtcggatctccatcaccagtgatctacgcctgg...
:ggattactgggccaaggacttcggtcctgagccagtgacctgagccagtgcccatcgtctcatccacctgccctgtgtgtggagatacaagcccctcctcggtgactctaggatgc
:ggtcaaggtgtattccctgagcacctggccaccttgccagcctgcccatcaatgctgagtcttcatctccctccaaagatcaagaactgagccccacaatcaagccctgtcctcca
:tgtaacctcgagcacctggccaccttgg...
:caaatgccccaccagatgtccagatcagctggtttgtgaacaacgtggaagtacaacaccataggtacaacaaccatcagagagaaccatccagcgcccatcaatgctgagacttcatgtctgaacaacgtggagagtggaaaacagagctaaac
:cttgcctccaccagagaagaagatgtctgacctctgatggtcttactcatgtacagcaagctggtggtggaaagaaatagctactcctgttcagtggtcacgagggt
:gcacaatcaccacaccacgactaacagagcttctcccggactccgggtaaa

(1 light chain nucleotide sequence:

:ggtatccacacctcagtcctccagctgcttttctgatttctctgtattttgcttttctgttctgctctgttctctgttctctcagctctgttctctgttctctcagtctctgctgagtcttccagcagtgacacctgctgactcagtgttctccagcgtcctccagaggt
:ctgcagggccagtcagagcattggcacaagcatacagtggtatcagcaaagaacaaaatggttctcaaggcttctcatctgctctcatcaaagtatgctctacttcctcctctgatggt
:jtggcagtggatcaggggacagatttact...
:ggaaataaacggctgatgctgcaccaactgtatccatctcccaccatcgagagcttaacatctgaggtgctcagtcgtgctcttgaacaactctacccaaagacatc
:tgtcaagtggaagattgatggcagtgaacagtggactgatcaggaacagcacagacagctacacgctcaagagtgtctaccaaggacgag
:tgaacgacataacagctataccctgtgaggccactcaccattgtcaagagcttcaacaggaatgagtgt

FIG. 4B

CHIR-R1X Light Chain Risk Assignments

V-Region	Amino Acids 1-52
Risk	LHLHLHLHLMLLMLHLHLHLHMHHHHHHHHHHMHLMLLMHMHHHHHHH
Mouse	DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH----WYQQRTNGSPRLLIKYAS

V-Region	Amino Acids 53-109
Risk	HLMMLHMLMHLHLHLHLHLLLHLHLLHLHHHHHHHHHHHHHHHHLHHLHLLLLLL
Mouse	RSISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA

FIG. 4C

CHIR-RX1 Heavy Chain Risk Assignments

V-Region	Amino Acids 1-57
Risk	MHLHLHLHMLLMLLLHLHLHMHHHHHHHHHMHLMLLMHMHHHHHHHHHHH
Mouse	DVQLQESGPGLVKPSQSLSLTCTVT DYSITSDYAWN-WIR QFPGNKLEWMGYIS---YSGST

V-Region	Amino Acids 58-113
Risk	HMHMHMLMLMLHLHLHLMLLHLHLHLLLHLLHLHMHHHHHHHHHHHHHHHHHHHHLHLHLHLL
Mouse	SYNPSLKSRISITRDT SKNQFFLQLNSVTTEDTAT YYCASFDYAHAM-------DYWGQGTSVTVSS

FIG. 5A
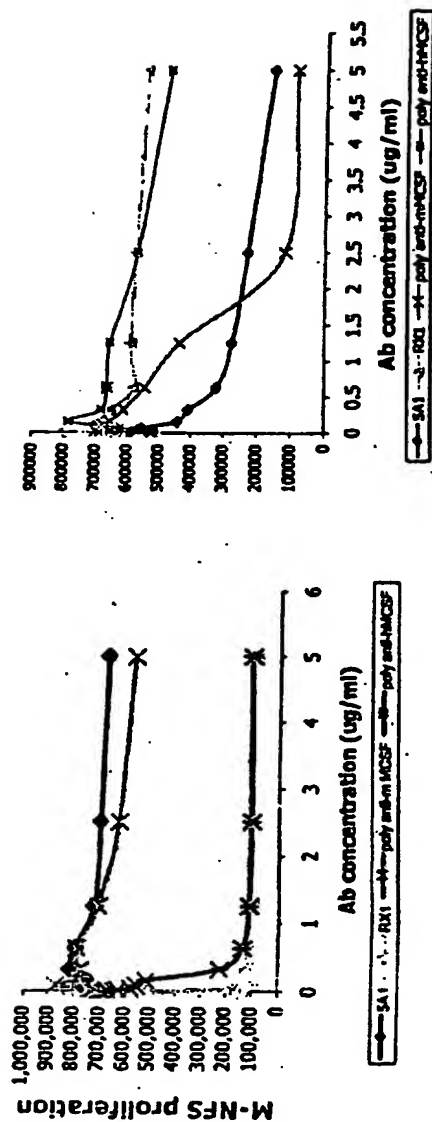
MC1 Neutralizes human MCSF activity
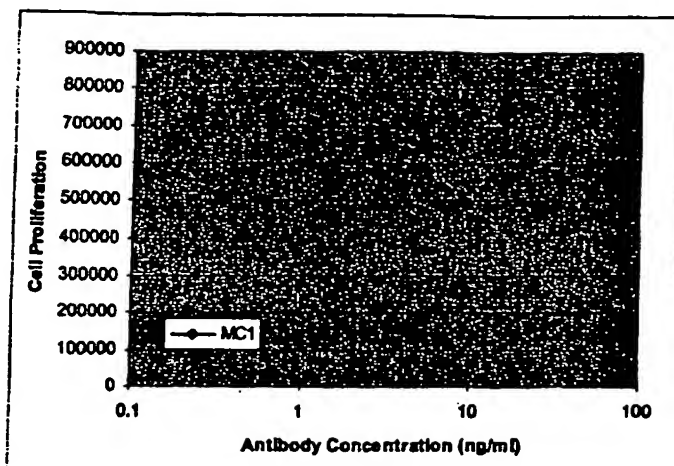
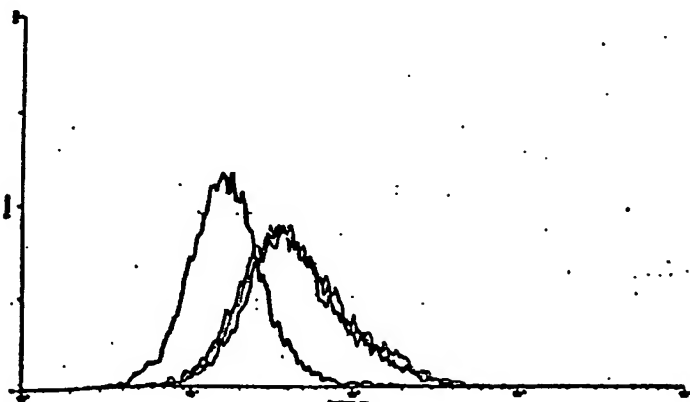## MC3 Neutralizes human MCSF activity
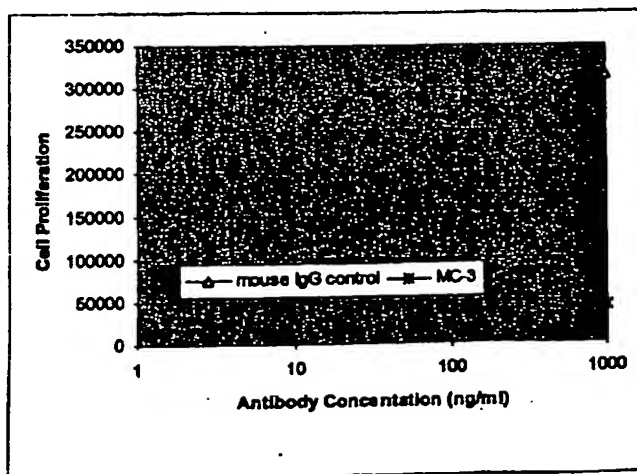
Fig. 6
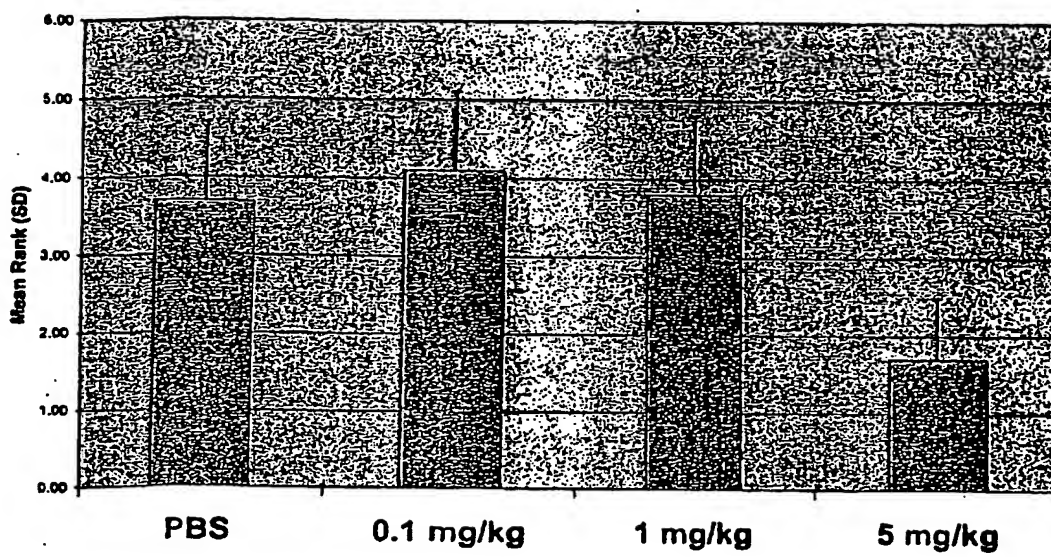
Fig. 7
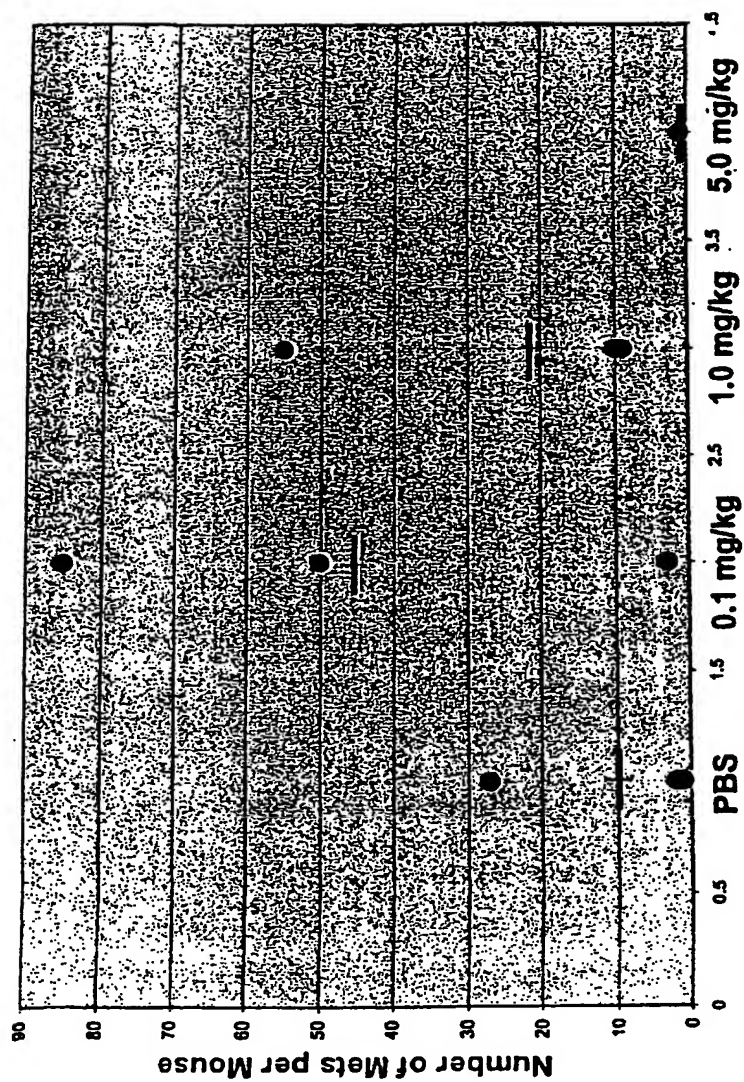
FIG. 8A

Binding of MCSF-specific antibody to breast cancer cell line MDA231

Red: no antibody control
Black: M-CSF antibody 1 ug/ml
Green: M-CSF antibody 10 ug/ml
Blue: M-CSF antibody 50 ug/ml

FIG. 8B

Binding of MCSF-specific antibody to multiple myeloma cancer cell line ARH77

Red: no antibody control
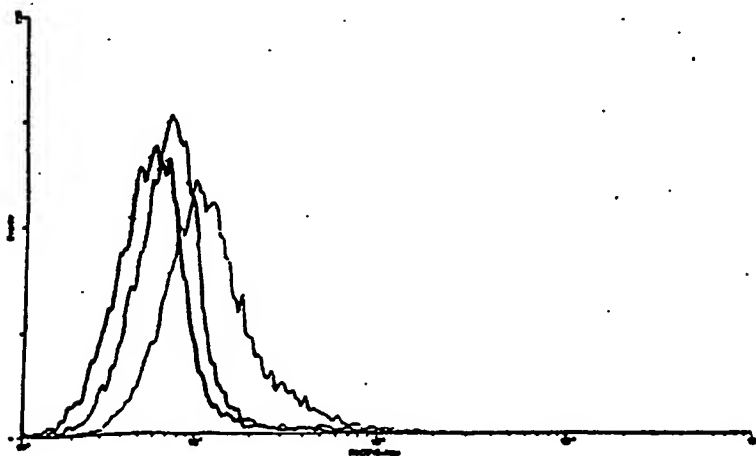Green: M-CSF antibody 5 ug/ml
Blue: control IgG2a 5 ug/ml

FIG. 9

Cancer Type	Cancer Status	Score 0	Score 1	Score 2	Score 3	Score 4	% with scores 3 or higher
adrenal	normal	10	5	5	0	0	0
basal cell	cancer	5	0	0	0	0	0
bladder	normal	6	1	2	1	0	10
brain	normal	17	1	2	0	0	0
breast	cancer	6	5	13	62	0	72
breast	normal	7	5	7	6	0	24
carcinoids	cancer	9	2	2	0	0	0
carcinoids (muscle)	cancer	1	0	1	0	0	0
choriocarcinoma	cancer	1	0	0	0	0	0
colon	normal	4	0	2	0	0	0
colon	cancer	9	0	1	4	0	27
fibrosarcoma	cancer	3	1	0	0	0	0
gallbladder	normal	2	1	0	1	0	25
germ cell	cancer	1	0	0	0	0	0
heart	normal	7	3	2	4	0	25
kidney	normal	5	10	1	4	0	20
kidney	cancer	8	1	0	3	0	25
leiomyosarcoma	cancer	5	0	0	0	0	0
liver	normal	11	3	4	1	0	6
liver	cancer	5	3	0	3	0	27
lung	normal	19	0	1	0	0	0
lung	cancer	3	1	0	3	0	43
lymphoma	cancer	13	0	3	2	0	12
melanoma	cancer	7	0	2	5	0	36
melanoma(inflammation)	cancer	0	0	0	1	0	100
mesothelioma	cancer	6	0	0	0	0	0
neuroblastoma	cancer	1	0	0	0	0	0
ovary	normal	6	0	2	0	0	0
ovary	cancer	8	2	0	4	0	29
pancreas	normal	9	2	5	4	0	20
pancreas	cancer	8	1	0	3	0	25
prostate	normal	0	3	8	3	0	21
prostate	cancer	9	1	1	4	0	27
sarcoma all	cancer	6	0	2	2	0	20
sarcoma	cancer	3	0	2	1	0	17
sarcoma (kidney)	cancer	3	0	2	1	0	17
sarcoma mfh	cancer	2	0	0	0	0	0
seminoma	cancer	3	0	0	0	0	0
small intestine	normal	2	1	0	1	0	25
spleen	normal	14	2	3	0	0	0
squamous cell	cancer	3	0	0	0	0	0
stomach	normal	3	2	2	1	0	13
stomach	cancer	7	1	1	1	0	10
teratoma	cancer	1	0	0	0	0	0
testis	normal	5	1	3	3	0	25
thyroid	normal	15	0	0	0	0	0
thyroid	cancer	6	2	1	2	0	18
undiff all	cancer	6	0	2	1	0	11
undif	cancer	5	0	2	0	0	0

Fig. 10

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1             5             10            15

Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
            20            25            30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35            40            45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50            55            60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65            70            75            80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
            85            90            95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100           105           110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
    115           120           125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130           135           140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145           150           155           160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
            165           170           175

Glu Cys Ser Ser Gln Gly His Glu Arg Gln Ser Glu Gly Ser Ser Ser
            180           185           190

Pro Gln Leu Gln Glu Ser Val Phe His Leu Leu Val Pro Ser Val Ile
    195           200           205

Leu Val Leu Leu Ala Val Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg
    210           215           220

Arg Ser His Gln Glu Pro Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro
225           230           235           240

Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg Gln Val Glu Leu Pro Val
            245           250           255
```

Fig. 11

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1             5             10            15
Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
        20            25            30
Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35            40            45
Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50            55            60
Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65            70            75            80
Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
            85            90            95
Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
        100           105           110
Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
    115           120           125
Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130           135           140
Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145           150           155           160
Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
            165           170           175
Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
        180           185           190
Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
        195           200           205
Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
    210           215           220
Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225           230           235           240
Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
            245           250           255
Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
        260           265           270
Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
        275           280           285
Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
    290           295           300
Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305           310           315           320
Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
            325           330           335
Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
        340           345           350
Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala Leu Pro
        355           360           365
Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His Thr Pro
    370           375           380
Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
385           390           395           400
Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Gly Leu Ser Asn Pro
            405           410           415
Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
        420           425           430
Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
        435           440           445
Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala
    450           455           460
Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
465           470           475           480
His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
            485           490           495
Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
        500           505           510
Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
        515           520           525
Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
    530           535           540
Gln Asp Asp Arg Gln Val Glu Leu Pro Val
```

Fig. 12

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1           5               10          15
Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
        20              25          30
Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35              40          45
Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50              55          60
Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65              70          75          80
Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
            85          90          95
Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
        100         105         110
Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115         120         125
Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
        130         135         140
Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145             150         155         160
Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
            165         170         175
Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
        180         185         190
Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
        195         200         205
Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
    210         215         220
Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225             230         235             240
Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
            245         250         255
Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
        260         265         270
Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
        275         280         285
Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
    290         295         300
Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305         310         315         320
Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
        325         330         335
Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
        340         345         350
Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly His Glu Arg Gln
        355         360         365
Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu
    370         375         380
Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu
385         390         395         400
Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp
            405         410         415
Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg
        420         425         430
Gln Val Glu Leu Pro Val
```

FIG. 13

5H4 heavy chain protein sequence:

```
  1   EIQLQQSGPE LVKTGTSVKI SCKASGYSFT GYFMHWVKQS HGKSLEWIGY
 51   ISCYNGDTNY NQNFKGKATF TVDTSSSTAY MQFNSLTSED SAVYYCAREG
101   GNYPAYWGQG TLVTVSAAKT TPPSVYPLAP GSAAQTNSMV TLGCLVKGYF
151   PEPVTVTWNS GSLSSGVHTF PAVLQSDLYT LSSSVTVPSS TWPSETVTCN
201   VAHPASSTKV DKKIVPRDCG CKPCICTVPE VSSVFIFPPK PKDVLTITLT
251   PKVTCVVVDI SKDDPEVQFS WFVDDVEVHT AQTQPREEQF NSTFRSVSEL
301   PIMHQDWLNG KEFKCRVNSA AFPAPIEKTI SKTKGRPKAP QVYTIPPPKE
351   QMAKDKVSLT CMITDFFPED ITVEWQWNGQ PAENYKNTQP IMDTDGSYFV
401   YSKLNVQKSN WEAGNTFTCS VLHEGLHNHH TEKSLSHSPG K
```

5H4 light chain protein sequence:

```
  1   DIVMTQSHKF MSTSVGDRVT ITCKASQNVG TAVTWYQQKP GQSPKLLIYW
 51   TSTRHAGVPD RFTGSGSGTD FTLTISDVQS EDLADYFCQQ YSSYPLTFGA
101   GTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
151   DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201   STSPIVKSFN RNEC
```

FIG. 14

MC-1 heavy chain protein sequence:

```
  1    EVKLVESGGG  LVQPGGSLKL  SCATSGFTFS  DYYMYWVRQT  PEKRLEWVAY
 51    ISNGGGSTYY  PDTVKGRFTI  SRDNAKNTLY  LQMSRLKSED  TAMYYCARQG
101    SYGYPFAYWG  QGTLVTVSAA  KTTAPSVYPL  APVCGDTTGS  SVTLGCLVKG
151    YFPEPVTLTW  NSGSLSSGVH  TFPAVLQSDL  YTLSSSVTVT  SSTWPSQSIT
201    CNVAHPASST  KVDKKIEPRG  PTIKPCPPCK  CPAPNLLGGP  SVFIFPPKIK
251    DVLMISLSPI  VTCVVVDVSE  DDPDVQISWF  VNNVEVHTAQ  TQTHREDYNS
301    TLRVVSALPI  QHQDWMSGKE  FKCKVNNKDL  PAPIERTISK  PKGSVRAPQV
351    YVLPPPEEEM  TKKQVTLTCM  VTDFMPEDIY  VEWTNNGKTE  LNYKNTEPVL
401    DSDGSYFMYS  KLRVEKKNWV  ERNSYSCSVV  HEGLHNHHTT  KSFSRTPGK
```

MC-1 light chain protein sequence:

```
  1    AIQMTQTTSS  LSASLGDRVT  ISCSASQGIS  NYLNWYQQKP  DGTVKLLIYY
 51    TSSLHSGVPS  RFSGSGSGTD  YSLTISNLEP  EDIATYYCQQ  YSKLPWTFGG
101    GTKLEIKRAD  AAPTVSIFPP  SSEQLTSGGA  SVVCFLNNFY  PKDINVKWKI
151    DGSERQNGVL  NSWTDQDSKD  STYSMSSTLT  LTKDEYERHN  SYTCEATHKT
201    STSPIVKSFN  RNEC
```

FIG. 15

MC-3 heavy chain protein sequence:

```
  1   DVQLQESGPG LVKPSQSLSL TCTVTGYSIT SDYAWNWIRQ FPGNKLEWMG
 51   YISYSGSTSY NPSLKSRISI TRDTSKNQFF LQLNSVTTED TATYYCARLE
101   TWLFDYWGQG TTLTVSSAKT TPPSVYPLAP GCGDTTGSSV TLGCLVKGYF
151   PESVTVTWNS GSLSSSVHTF PALLQSGLYT MSSSVTVPSS TWPSQTVTCS
201   VAHPASSTTV DKKLEPSGPI STINPCPPCK ECHKCPAPNL EGGPSVFIFP
251   PNIKDVLMIS LTPKVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQTQTHRE
301   DYNSTIRVVS TLPIQHQDWM SGKEFKCKVN NKDLPSPIER TISKIKGLVR
351   APQVYILPPP AEQLSRKDVS LTCLVVGFNP GDISVEWTSN GHTEENYKDT
401   APVLDSDGSY FIYSKLNMKT SKWEKTDSFS CNVRHEGLKN YYLKKTISRS
451   PGLDLDDICA EAKDGELDGL WTTITIFISL FLLSVCYSAS VTLFKVKWIF
501   SSVVELKQKI SPDYRNMIGQ GA
```

MC-3 light chain protein sequence:

```
  1   DILLTQSPAI LSVSPGERVS FSCRASQSIG TSIHWYQQRT NGSPRLLIKY
 51   ASESISGIPS RFSGSGSGTD FTLSINSVES EDIADYYCQQ SNSWPTTFGG
101   GTKLEIKWAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
151   DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201   STSPIVKSFN RNEC
```

FIG. 16A

For heavy chain CDR1:

```
                         1
      H_CDR1_5H4    (1)  -GYFMH
      H_CDR1_MC-1   (1)  -SYYMY
   H_CDR1_CHIR-RX1  (1)  SDYAN
      H_CDR1_MC-3   (1)  SDYAN
      Consensus     (1)  SDYAWN
```

For heavy chain CDR2:

```
                         1               17
      H_CDR2_5H4    (1)  YISCENGDTNYNQNFKG
      H_CDR2_MC-1   (1)  YISNGGGTYYPD KG
   H_CDR2_CHIR-RX1  (1)  YIS-SGTSYNPSLK
      H_CDR2_MC-3   (1)  YIS-SGTSYNPSLK
      Consensus     (1)  YIS YSGSTSYNPSLKS
```

For heavy chain CDR3:

```
                         1
      H_CDR3_5H4    (1)  --GNYPAY
      H_CDR3_MC-1   (1)  QGS  PAY
   H_CDR3_CHIR-RX1  (1)  -F  HAM Y
      H_CDR3_MC-3   (1)  --LETL  Y
      Consensus     (1)   DYGW FDY
```

FIG. 16B

For light chain CDR1:

```
                            1              11
     L_CDR1_5H4      (1)   ░ASON░░░░░T
     L_CDR1_MC-1     (1)   SASOG░SNY░N
  L_CDR1_CHIR-RX1    (1)   ░ASO░░░░░░
     L_CDR1_MC-3     (1)   ░ASO░░░░░░
        Consensus    (1)   RASQSIGTSIH
```

For light chain CDR2:

```
                            1
     L_CDR2_5H4      (1)   ░░STRH░
     L_CDR2_MC-1     (1)   ░░SLH░
  L_CDR2_CHIR-RX1    (1)   ░AS░░░░
     L_CDR2_MC-3     (1)   ░AS░░░░
        Consensus    (1)   YTSESIS
```

For light chain CDR3:

```
                            1
     L_CDR3_5H4      (1)   QQ░░░░PLT
     L_CDR3_MC-1     (1)   QQ░KLPW░
  L_CDR3_CHIR-RX1    (1)   QQIN░░P░T
     L_CDR3_MC-3     (1)   QQSN░░P░T
        Consensus    (1)   QQYSSWPTT
```

FIG. 17

Neutralization Activities of Intact mAbs vs. Fabs
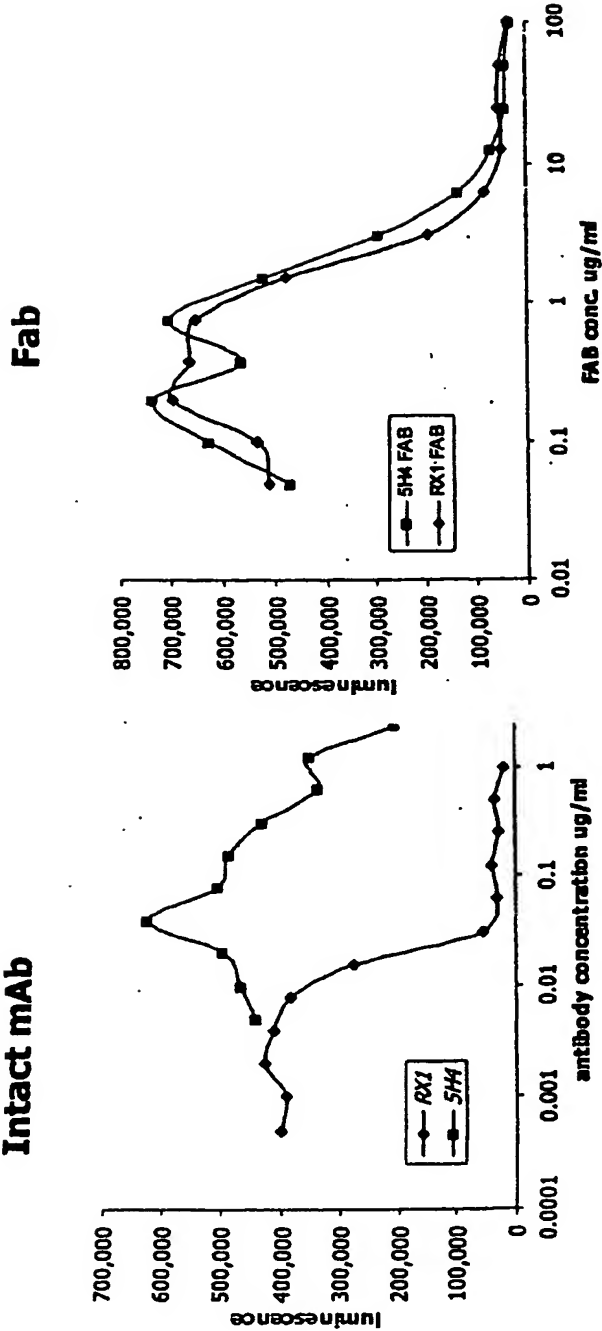
FIG. 18

MCSF Structure with RX1 Epitopes Highlighted

RX1

R$_{98}$FRDNTPN$_{105}$

5H4

I$_{65}$TFEFVDQE$_{73}$

MC3

I$_{65}$TFEFVDQE$_{73}$

F$_{138}$YETPLQ$_{144}$

FIG. 19A

Heavy Chain

V-Region	No.of Changes	Amino Acids 1-57
Risk		MHLHLHLHMLLMLLLHLHLHMHHHHHHHHHHMHLLLMHMHHHHHHHHHHHH
Mouse		DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWN-WIRQFPGNKLEWMGYIS---YSGST
Human		qvqLqesGpgLvKPsqTLsLTCxvsGxsxSsxxxxxWiRQpPgkgLEWigxiyyraxxgxt
Low Risk	2	DVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWN-WIRQFPGKKLEWMGYIS---YSGST
Low+Mod	5	QVQLQESGPGLVKPSQTLSLTCTVSDYSITSDYAWN-WIRQFPGKGLEWMGYIS---YSGST

V-Region	No.of Changes	Amino Acids 58-113
Risk		HMHMMHMLHLHLHLMLLMLHLHLLHLHLLHLMHHHHHHHHHHHHHHHHLHHLHLHLL
Mouse		SYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDYAHAM-------DYWGQGTSVTVSS
Human		xynpSlksRvTisvDTSKNQfsLxlxsvtaaDTAvYyCArxxxxxxxxxxxxfdxWGgGtxVTVSS
Low Risk	6	SYNPSLKSRITISRDTSKNQFSLQLNSVTAADTATYYCASFDYAHAM-------DYWGQGTTVTVSS
Low+Mod	7	SYNPSLKSRITISRDTSKNQFSLQLNSVTAADTAVYYCASFDYAHAM-------DYWGQGTTVTVSS

FIG. 19B

Low Risk Heavy Chain Vs. Kabat Vh2 Consensus:

Protein Seq:

DVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWNWIRQFPGKLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSLQLNSVTAADTATYYCASFDYAHAMD
YWGQGTTVTVSS

DNA Seq:

GACGTACAACTTCAAGAATCTGGCCCAGGTCTGTCGTCAAACCTCTCAAACCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCGACTACGCTT
GGAACTGGATCCGACAATTTCCTGGTAAAAACTGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCTCTTACAATCCTTCTGAAATCACGGATCAC
AATTTCCGGCGATACCTCTAAAAATCAATTTCACTCCAACTCAATTCTGTTACCGGCCGATACTGCCAACTCACTGTGCCTCTTTTGACTACGCTCACG
CCATGATTATTGGGGACAGGGTACTACCGTTACCGTAAGCTCA

Low Risk + Moderate Risk Heavy Chain Vs. Kabat Vh2 Consensus:

Protein Seq:

QVQLQESGPGLVKPSQTLSLTCTVSDYSITSDYAWNWIRQFPGKGLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSLQLNSVTAADTAVYYCASFDYAHAMD
YWGQGTTVTVSS

DNA Seq:

CAAGTTCAACTTCAAGAATCAGGCCCGGACTCGTTAAACCCTCTCAAACTCTCTCTTACTTGCACTGTATCCGATTACTCTATTACTTCAGACTACGCTTG
GAACTGGATCAGACAATTTCCCGGAAAAGGACTCGAAATGGATGGGATATATCTTACTCTGGCTCAACCTCTTACAACCCTCTCTCAAATCTCGAATAAC
AATCTCACGCGATACTTCTAAAAATCAATTCTCACTTCAACTTAACTCCGTTACTGCCGCCGACACTGCGTTACTACTGGCTTCCTTCGATTACGCCCACG
CTATGGATTATTGGGGACAAGGAACTACCGTCACTGTCAGCTCA

FIG. 20A

Light Chain

V-Region	No. of Changes	Amino Acids 1-52
Risk		LHLHLHLHLMLLMLLHLMLLHLHLHLHMHHHHHHHHHMHLMLLMHMHHHHHH
Mouse		DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH---WYQQRTNGSPRLLIKYAS
Human		EIV1TQSPgTLS1SPGERaTLSCRASQSvssyL---AWYQQkPGQAPRLLIYgAS
Low Risk	8	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH---WYQQKTGQSPRLLIKYAS
Low+Mod	9	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH---WYQQKTGQAPRLLIKYAS

V-Region	No. of Changes	Amino Acids 53-109
Risk		HLMMLHMLMHLHLHLLHLLLHLLHHHHHHHHHHHHHHHHHLHHLHLLLLLL
Mouse		ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT-----TFGGGTKLEI-KRA
Human		sRATGIPdRFSGSGSGTDFTLTISrLepEDFAVYYCQQygsspp----xTFGgGTKvEI-KRT
Low Risk	8	ERISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT-----TFGQGTKLEI-KRT
Low+Mod	10	ERATGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT-----TFGQGTKLEI-KRT

FIG. 20B

Low Risk Light Chain Vs. Kabat Vk3 Consensus:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQSPRLLIKYASERISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTCCTTACCCAATCTCCCGGAACCCTCTCAGTATCTCCCGGGAACGAGTAACCTTTCATGTAGAGAGCATCCCAATCCATCGGCACTTCAATTCACTGGTATCAGCAGAAAACAGGTCAATCCCCACGGCTTCTTATAAAATATGCATCAGAAAGAATATCAGACAGATTCAGGTTCAGGTTCAGGCACAGACTTCACACTTACAATTTCCCGGCGTCGAATCCGAAGACTTCGCTGACTATTACTGCCAACAAATCAACTCATGGCCTACTTTCGGTCAAGGCACCAAACTCGAAATTAAACGTACG

Low Risk + Moderate Risk Light Chain Vs. Kabat Vk3 Consensus:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQAPRLLIKYASERATGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTTCTTACTCAATCCCCGGTACACTCTCAGTTTCCCCAGGCGAACGGTCACTTTTCTTGCAGAGCATCACAATCAATCGGCACTTCAATTCATTGGTATCAACAAAAACAGGACAGGGCCCACGACTTCTTATTAAATATGCATCAGAAACGAGCCACAGGCATCCAGACAGATTTTCAGGTTCAGGATCAGGCACCGATTTCACACTTCACATATCCAGAGTCGAATCAGAAGATGTCAACAAATAAACAGCTGGCCCACTACATTCGGACAAGGCACAAAACTCGAAATTAAACGTACG

FIG. 21A

Light Chain – Changes back to Murine

V-Region	No.of Changes	Amino Acids 1-52
Risk		LHLHLHLHLMLLMLLHLHLHLHLMHHHHHHHMHLLMHMHHHHHH
Mouse		DILLTQSPAILSVSPGERVSFSCRASQSIGTSIH---WYQQRTNGSPRLLIKYAS
Human		EIVlTQSPgTLSlSPGERaTLSCRASQSvssyL--AWYQQkPGQAPRLLIYgAS
Low Risk	8	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH---WYQQKTGQSPRLLIKYAS
Low+Mod	9	EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIH---WYQQKTGQAPRLLIKYAS

V-Region	No.of Changes	Amino Acids 53-109
Risk		HLMMLHMLMHLHLHLHLHLLHLHHHHHHHHHHHHHHHLHHLHLHLLLLLL
Mouse		ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA
Human		sRATGIPdRFSGSGSGTDFTLTISrLepEDFAVYYCQQygsspp----xTFGqGTKvEI-KRT
Low Risk	8	ERISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT
Low+Mod	10	ERATGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT
Low+Mod Altnernate	7	ESISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPT------TFGQGTKLEI-KRT

FIG. 21B

Low Risk Light Chain Vs. Kabat Vk3 Consensus; AA54 changed back to murine:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQSPRLLLIKYASESISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTCCTTACCCAATCTCCCGGAACCCTCTCAGTATCTCCCGGCGAACGAGTAACCTTTCATGTAGAGCATCCCAATTCACT
GGTATCAGCAGAAAAACAGGTCAATCCCCACGGCTTCTTATAAAATATGCATCCCAGACAGATTTCAGGTTCAGGATCAGGCA
CCGATTTCACACTTCACAATATCCAGAGTCGAATCAGAAGATTTTGCAGATTACTATTGTCAACAAATAAACAGCTGGCCCACTACATTCGGACAAGGCACAA
AACTCGAAATTAAACGTACG

Low Risk + Moderate Risk Light Chain Vs. Kabat Vk3 Consensus; AA54, 55, 56 changed back to murine:

Protein Seq:

EIVLTQSPGTLSVSPGERVTFSCRASQSIGTSIHWYQQKTGQAPRLLLIKYASESISGIPDRFSGSGSGTDFTLTISRVESEDFADYYCQQINSWPTTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTTCTTACTCAATCCCCCGGTACACTCTCAGTTCCCCAGGCGAACGCGTCACTTTTCTTGCAGAGCATCACAATCAATCGGCACTTCAATTCATT
GGTATCAACAAAAAACAGGACAGGCCCACGACTTCTTATTAAATATGCATCCCAGACAGATTTCAGGTTCAGGATCAGGCA
CCGATTTCACACTTCACAATATCCAGAGTCGAATCAGAAGATTTTGCAGATTACTATTGTCAACAAATAAACAGCTGGCCCACTACATTCGGACAAGGCACAA
AACTCGAAATTAAACGTACG

FIG. 22A

Light Chain – Changes based on HK6 2-1-1(A14)

V-Region	No.of Changes	Amino Acids 1-52
Risk		LHLHLHLMLLHLMLLLHLHLHMHHHHHHHHHMHLMLLMHMHHHHHH
Mouse		DFLLTQSPAILSVSPGERVSFSCRASQSIGTSIH----WYQQRTNGSPRLLIKYAS
Human		DVVMTQSPAFLSVTPGEKVTITCQASEGIGNYLY----WYQQKPDQAPKLLIKYAS
Low Risk	10	DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIH----WYQQKTDQSPRLLIKYAS
Low+Mod	12	DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIH----WYQQKTDQAPKLLIKYAS

V-Region	No.of Changes	Amino Acids 53-109
Risk		HLMLMLHMLHLHLHLHLHLLHLHLLLHHHHHHHHHHHHHLHLHLHLLLLLLL
Mouse		ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT-----TFGGGTKLEI-KRA
Human		QSISGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQGNKHP-----LTFGGGTKVEI-KRT
Low Risk	5	ESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQINSWPT-----TFGGGTKLEI-KRT
Low+Mod	5	ESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQINSWPT-----TFGGGTKLEI-KRT

FIG. 22B

Low Risk Light Chain vs. VK6 Subgroup 2-1-(1) A14:

Protein Seq:

DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIHWYQQKTDQSPRLLIKYASESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQINSWPTTFGGGTKLEIKRT

Nucleotide Seq: Not synthesized

Low Risk + Moderate Risk Light Chain vs. VK6 Subgroup 2-1-(1) A14:

DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIHWYQQKTDQAPKLLIKYASESISGIPSRFSGSGSGTDFTLTISSVEAEDAADYYCQQI
NSWPTTFGGGTKLEIKRT

Nucleotide Seq:

GACATAGTTCTCACACAATCACCAGCATTCCTCCTCAGTTACACCCGGGCGAAAAAGTAACCTTTACCTGTCAGCTTCTCAATCTATCGGGCACTTCTATTCACT
GGTATCAACAAAAAACCGATCAAGCTCCTAAACTCCTCATAAACTCCTCATAAATACGCATCCGAATCCATCCGGTATCCCTCCGGTATCCCTCCGATTTTCAGGCTCCGGTCCGGCA
CAGATTTCACCCTTACCATTAGCTCAGTTGAAGCCGAAGACGCAGCTGATTACTACTGTCAACAAATAAACTCATGCCCACTACTTTCGGCGGCGGCGGCACTA
AACTCGAAATAAAACGTACG

FIG. 23A

Murine RX-1 Light Chain:

DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPTTFGGGTK
LEIKRA

RX1 KV	(1)	DILLTQSPAILSVSPGERVSFSCRASQSIGT-S----IHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPTTFG
Consensus Germline LC		
hVK I Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQSISS-Y----LNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP----
hVK II Consensus	(1)	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLLIYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEP----
hVK III Consensus	(1)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSY----LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP----
hVK IV Consensus	(1)	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP----
hVK V Consensus	(1)	ETTLTQSPAFMSATPGDKVNISCKASQDIDD-D----MNWYQQKPGEAAIFIIQEATLVPGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP----
hVK VI Consensus	(1)	EIVLTQSPDFQSVTPKEKVTITCRASQSIGS-S----LHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSLP----

---

LIGHT CHAIN amino half

RX-1	DILLTQSPAILSVSPGERVSFSCRASQSI--GTSIH----WYQQRTNGSPRLLIKYAS
pos...	10 20 abcdef 30 40 50

Kabat:

HK1	DIQMTQSPSSLSASVGDRVTITCRASQSLVXX-XISXXLXWYQQKPGKAPKLLIYAAS
HK2	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSXDGXXYLNWYLQKPGQSPQLLIYXXS
HK3	EIVLTQSPGTLSLSPGERATLSCRASQS----VSSSYLAWYQQKPGQAPRLLIYGAS
HK4	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWAS

Germline Consensus (with JK4):

hVK1	DIQMTQSPSSLSASVGDRVTITCRASQS-------ISSYLNWYQQKPGKAPKLLIYAAS
hVK2	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLLIYTLS
hVK3	EIVLTQSPGTLSLSPGERATLSCRASQS----VSSSYLAWYQQKPGQAPRLLIYGAS
hVK4	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWAS
hVK5	ETTLTQSPAFMSATPGDKVNISCKASQDIDD-----DMNWYQQKPGEAAIFIIQEAT
hVK6	EIVLTQSPDFQSVTPKEKVTITCRASQSIG------SSLHWYQQKPDQSPKLLIKYAS

FIG. 23B

LIGHT CHAIN carboxy half

```
RX-1   ESISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQINSWPT------TFGGGTKLEI-KRA

pos...        60        70        80        90    abcdef 100    a

Kabat:

HK1...XLXSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQXXXPE-----XTFGQGTKVEI-KRT
HK2...NRXSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAXQXPR-----XTFGQGTKVEI-KRT
HK3...SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPP-----XTFGQGTKVEI-KRT
HK4...TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP------XTFGQGTKVEI-KRT

Germline Consensus (with JK4):

hVK1   SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP------LTFGGGTKVEI-KRT
hVK2   YRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP------LTFGGGTKVEI-KRT
hVK3   SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP------LTFGGGTKVEI-KRT
hVK4   TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP------LTFGGGTKVEI-KRT
hVK5   TLVPGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP------LTFGGGTKVEI-KRT
hVK6   QSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP------LTFGGGTKVEI-KRT
```

FIG. 24A

Murine RX-1 Heavy Chain:
DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYC
ASFDYAHAMDYWGQGTSVTVSS

```
RX1 VH           (1) D VQLQESGPGLVKPSQSLS LTCTVTDYSITS -DYAWNWIRQFPPGNKLEWMGYISYSGSTS --- YNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASPDY
Consensus Germline
hVH I Consensus  (1) QVQLVQSGAEVKPGASVKVSCKASGYTFTG -YYMHWVRQAPGQGLEWMGWINP -- NSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR --
hVH II Consensus (1) QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGWIRQPPGKALEWLALIYWNDDKR -- YSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHR --
hVH III Consensus(1) E VQLVESGGGLVQPGGSLRLSCAASGFTFSS -YWMSWVRQAPGKGLEWVANIKQ - DGSEKYYVDSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCAR --
hVH IV Consensus (1) QVQLQESGPGLVKPSGTLSLTCAVSGGSISSS -NWWSWVRQPPGKGLEWIGEIYHSGSTN --- YNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCAR --
hVH V Consensus  (1) E VQLVQSGAEVKKPGESLKISCKGSGYSFTS -YWIGWVRQMPGKGLEWMGIIYP - GDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR --
hVH VI Consensus (1) QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWYN - DYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAR --
hVH VII Consensus(1) QVQLVQSGSELKKPGASVKVSCKASGYTFTS -YAMNWVRQAPGQGLEWMGWINT - NTGNPTYAQGFTGRFVFSLDTSV STAYLQICSLKAEDTAVYYCAR --
```

HEAVY CHAIN amino half

```
          DVQLQESGPGLVKPSQSLSLTCTVTDYSITSDYAWN-WIRQFPGNKLEWMGYIS---YSGST

pos ...        10        20        30    ab    40    50   abc

Kabat:
```

```
HH1 ...XVQLVQSGAEVKKPGXSVKVSCKASGYTFXSYXIX--WVRQAPGQGLEWMGXIXPY-XXGXT
HH2 ...QVQLQESGPGLVKPSQTLSLTCXVSGXSXXXXXXWIRQPPGKGLEWIGXIYYRAXXGXT
HH3 ...EVQLVESGGGLVQPGGSLRLSCAASGFTFSXYXMX--WVRQAPGKGLEWVXIXXKXXGXXT
```

Germline Consensus (with JH4):
```
hVHI    QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMH--WVRQAPGQGLEWMGWINP--NSGGT
hVHII   QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGWIRQPPGKALEWLALIY---WNDDK
hVHIII  EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMS--WVRQAPGKGLEWVANIK--QDGSEK
hVHIV   QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWW-SWVRQPPGKGLEWIGEIY---HSGST
hVHV    EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIG--WVRQMPGKGLEWMGIIYP--GDSDT
hVHVI   QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYY-RSKWYN
hVHVII  QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMN--WVRQAPGQGLEWMGWINT--NTGNP
```

FIG. 24B

HEAVY CHAIN carboxy half

```
        SYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASFDYAHAM--------DYWGQGTSVTVSS

pos ... 60     70     80  abc    90     100abcdefghijk     110
```

Kabat:

```
HH1 ...NYAQKFQGRVTITXDXSTSTAYMELSSLRSXDTAVYYCARXXXXXXXXXXXXXDXXFDXWGQGTLVTVSS
HH2 ...XYNPSLKSRVTISVDTSKNQFSLXLXSVTAADTAVYYCARXXXXXXXXXXXXXXXFDXWGQGTXVTVSS
HH3 ...YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAXXXXXXXXXXXYXXFDXWGQGTLVTVSS
```

Germline Consensus (with JH4):

```
hVHI    NYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARXXXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHII   RYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHIII  YYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHIV   NYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHV    RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARXXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHVI   DYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARXXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
hVHVII  TYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCARXXXXXXXXXXXXXXXXXYFDYWGQGTLVTVSS
```

Figure 24C:

Kabat numbering of 5H4:

5H4 heavy chain protein sequence:

```
1-30:       EIQLQQSGPE LVKTGTSVKI SCKASGYSFT
31-35:      GYFMH
36-49:      WVKQSHGKSLEWIG
50-65:      YIS C (52A) YNGDTNY NQNFKG
66-94:      KATF TVDTSSSTAY MQF N (82A) S(82B) L(82C) TSED SAVYYCAR
95-102:     EGGNYPAY
103-437:    WGQG TLVTVSAAKT TPPSVYPLAP GSAAQTNSMV
TLGCLVKGYFPEPVTVTWNS GSLSSGVHTF PAVLQSDLYT LSSSVTVPSS TWPSETVTCN
VAHPASSTKV DKKIVPRDCG CKPCICTVPE VSSVFIFPPK PKDVLTITLT PKVTCVVVDI
SKDDPEVQFS WFVDDVEVHT AQTQPREEQF NSTFRSVSEL PIMHQDWLNG KEFKCRVNSA
AFPAPIEKTI SKTKGRPKAP QVYTIPPPKE QMAKDKVSLT CMITDFFPED ITVEWQWNGQ
PAENYKNTQP IMDTDGSYFV YSKLNVQKSN WEAGNTFTCS VLHEGLHNHH TEKSLSHSPG K
```

5H4 light chain protein sequence:

```
1-23:       DIVMTQSHKF MSTSVGDRVT ITC
24-34:      KASQNVG TAVT
35-49:      WYQQKPGQSPKLLIY
50-56:      WTSTRHA
57-88:      GVPD RFTGSGSGTD FTLTISDVQS EDLADYFC
89-97:      QQYSSYPLT
98-214:     FGAGTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
            DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
            STSPIVKSFN RNEC
```

Figure 24D:

Kabat numbering of MC1

MC-1 heavy chain protein sequence:

```
1-30:       EVKLVESGGG LVQPGGSLKL SCATSGFTFS
31-35:      DYYMY
36-49:      WVRQTPEKRLEWVA
50-65:      YIS N (52A) GGGSTYY PDTVKG
66-94:      RFTI SRDNAKNTLY LQM S (82A) R (82B) L (82C) KSED TAMYYCAR
95-102:     QGSYGYPFAY
103-449:    WG QGTLVTVSAA KTTAPSVYPL APVCGDTTGS SVTLGCLVKG YFPEPVTLTW
NSGSLSSGVH TFPAVLQSDL YTLSSSVTVT SSTWPSQSIT CNVAHPASST KVDKKIEPRG
PTIKPCPPCK CPAPNLLGGP SVFIFPPKIK DVLMISLSPI VTCVVVDVSE DDPDVQISWF
VNNVEVHTAQ TQTHREDYNS TLRVVSALPI QHQDWMSGKE FKCKVNNKDL PAPIERTISK
PKGSVRAPQV YVLPPPEEEM TKKQVTLTCM VTDFMPEDIY VEWTNNGKTE LNYKNTEPVL
DSDGSYFMYS KLRVEKKNWV ERNSYSCSVV HEGLHNHHTT KSFSRTPGK
```

MC-1 light chain protein sequence:

```
1-23:       AIQMTQTTSS LSASLGDRVT ISC
24-34:      SASQGIS NYLN
35-49:      WYQQKP DGTVKLLIY
50-56:      YTSSLHS·
57-88:      GVPS RFSGSGSGTD YSLTISNLEP EDIATYYC
89-97:      QQ YSKLPWT
98-214:     FGGGTKLEIKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT STSPIVKSFN.
RNEC
```

Figure 24E

Kabat numbering of MC3

MC-3 heavy chain protein sequence:

```
1-30:    DVQLQESGPG LVKPSQSLSL TCTVTGYSIT
31-35:   SDYAW N (35A)
36-49:   WIRQ FPGNKLEWMG
50-65:   YISYSGSTSY NPSLKS
66-94:   RISIT RDTSKNQFFL QL N (82A) S (82B) V (82C) TTEDT ATYYCAR
95-102:  LETWLFDY

103-522: WGQG TTLTVSSAKT TPPSVYPLAP GCGDTTGSSV TLGCLVKGYF PESVTVTWNS
         GSLSSSVHTF PALLQSGLYT MSSSVTVPSS TWPSQTVTCS VAHPASSTTV
         DKKLEPSGPI STINPCPPCK ECHKCPAPNL EGGPSVFIFP PNIKDVLMIS
         LTPKVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQTQTHRE DYNSTIRVVS
         TLPIQHQDWM SGKEFKCKVN NKDLPSPIER TISKIKGLVR APQVYILPPP
         AEQLSRKDVS LTCLVVGFNP GDISVEWTSN GHTEENYKDT APVLDSDGSY
         FIYSKLNMKT SKWEKTDSFS CNVRHEGLKN YYLKKTISRS PGLDLDDICA
         EAKDGELDGL WTTITIFISL FLLSVCYSAS VTLFKVKWIF SSVVELKQKI
         SPDYRNMIGQ GA
```

MC-3 light chain protein sequence:

```
1-23:    DILLTQSPAI LSVSPGERVS FSC
24-34:   RASQSIG TSIH
35-49:   WYQQRT NGSPRLLIK
50-56:   YASESIS
57-88:   GIPS RFSGSGSGTD FTLSINSVES EDIADYYC
89-97:   QQ SNSWPTT
98-214:  FGG GTKLEIKWAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI
         DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
         STSPIVKSFN RNEC
```

Fig. 25

Measurement of Neutralizing Activity of heRX1
With Different IgG Subclass Constant Regions
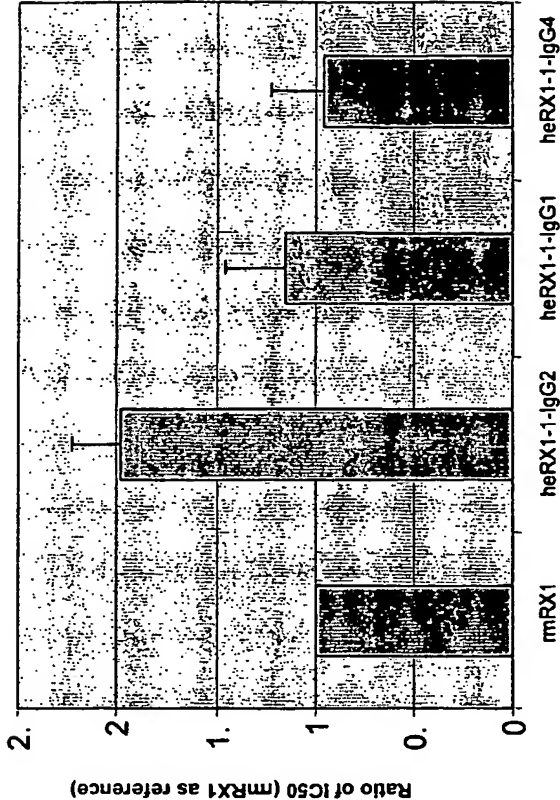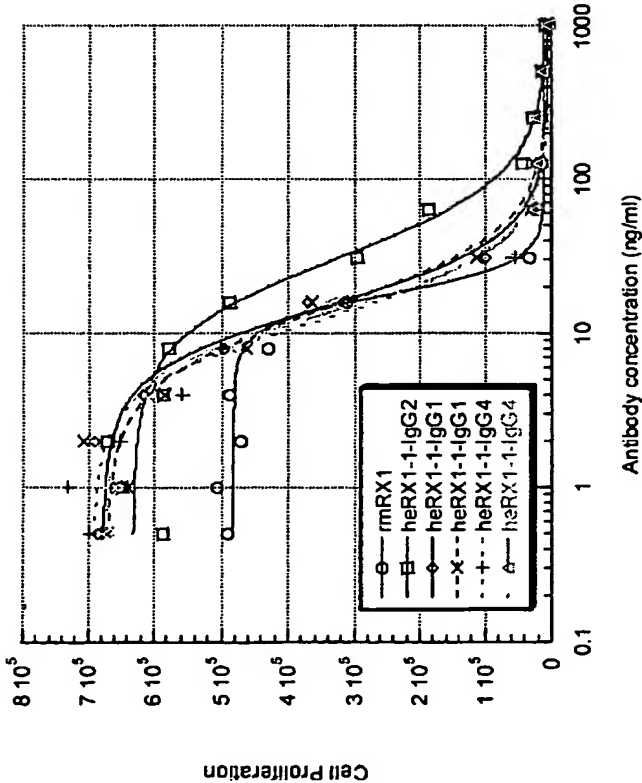
Against recombinant human MCSF

Fig. 26

Activity of heRX1-1 With Different IgG Subclasses Against Other Forms of MCSF

Neutralizing activity against human serum

Cell Proliferation / Antibody Concentration (ng/ml)

Legend: rmRX1 — RX1-1-IgG2 — RX1-1-IgG1 — RX1-1-IgG4 — RX2
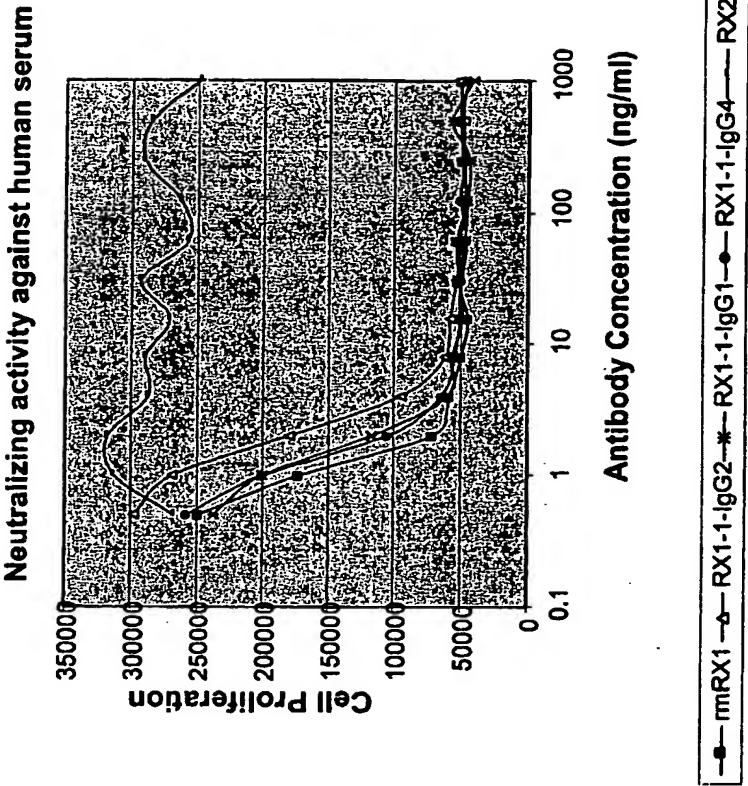
Similar results observed against Cyno MCSF in serum and recombinant Cyno MCSF

Fig. 27

Activity of heRX1-1 With Different IgG Subclasses Against Other Forms of MCSF
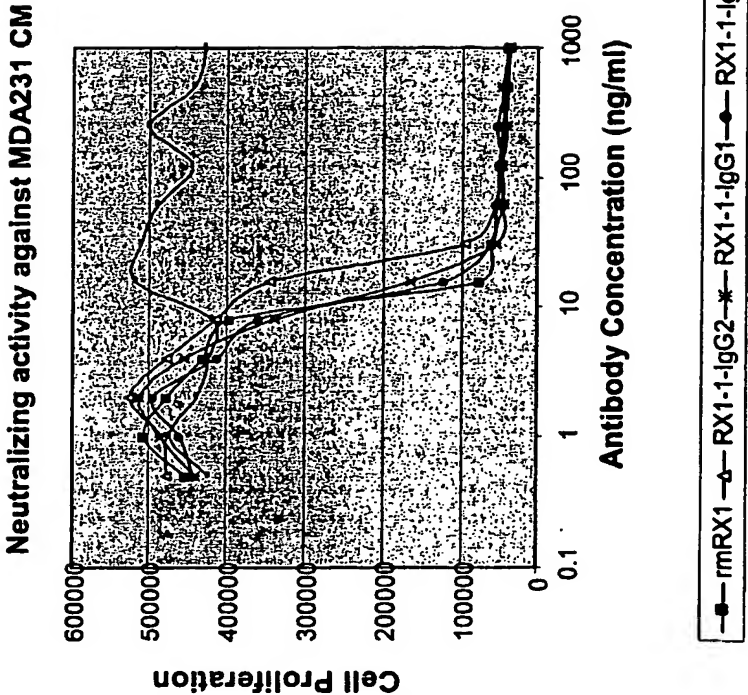
Similar results observed against Cyno MCSF in serum and recombinant Cyno MCSF

Fig. 28

Osteoclastogenesis Assay of heRX1-1 With Different IgG Subclasses
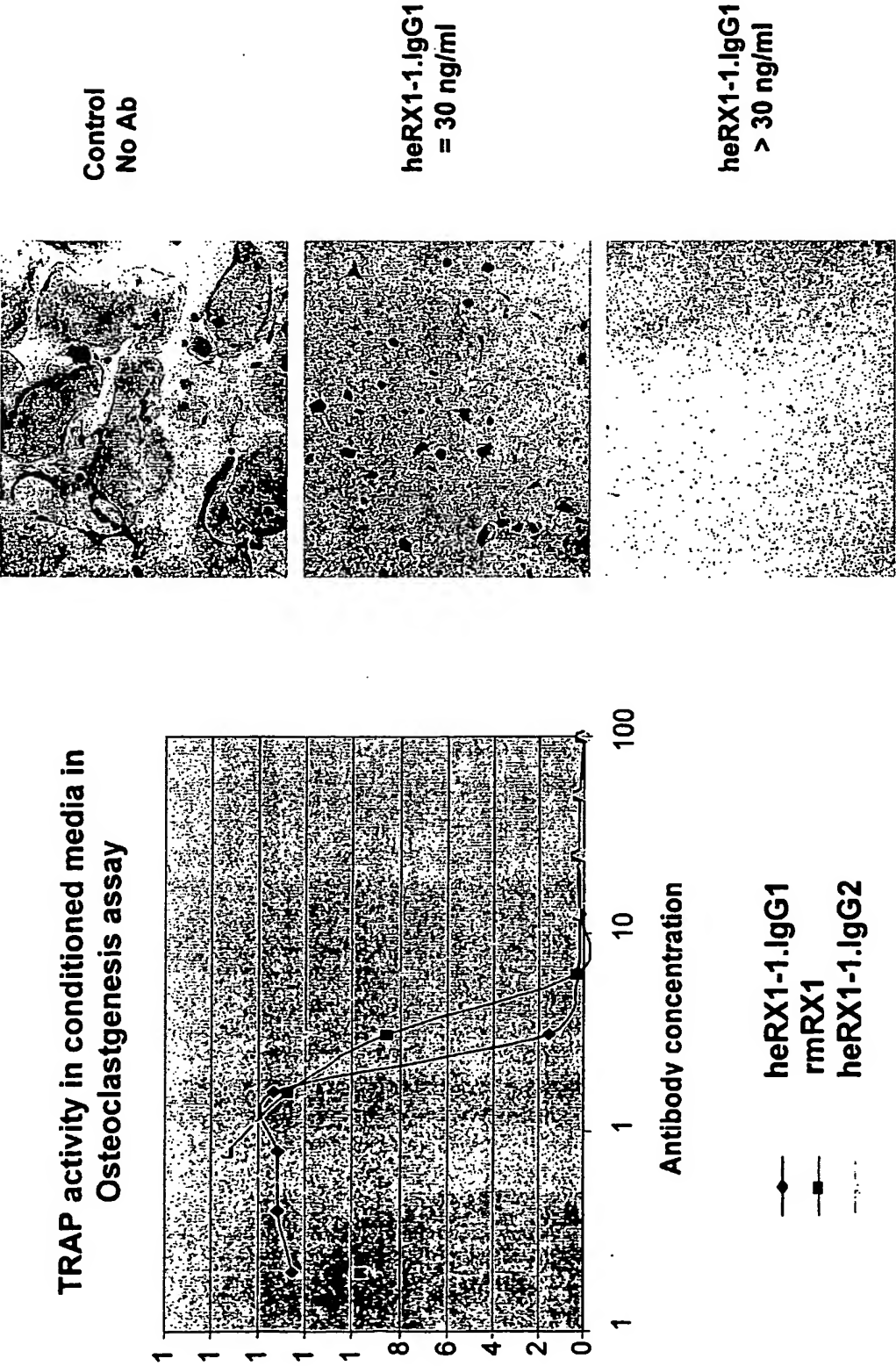
Amino Acids

MGWSCIILFLVATATGVHS

DVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWNWIRQFPGKKLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSL
QLNSVTAADTATYYCASFDYAHAMDYWGQGTTVTVSS

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPGK·

Nucleotides

ATGGGATGGAGTTGCATTATACTTTTCCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACTTCAAGAATC
TGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCT
CCTACAATCCTTCTCTGAAATCACGCATCACAATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA
CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGT
GGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGG
GGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
AGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
AGAGCCTCTCCCTGTCCCCGGGTAAATGA

Amino Acids

MGWSCIILFLVATATGVHS

QVQLQESGPGLVKPSQTLSLTCTVSDYSITSDYAWNWIRQFPGKGLEWMGYISYSGSTSYNPSLKSRITISRDTSKNQFSL
QLNSVTAADTAVYYCASFDYAHAMDYWGQGTTVTVSS

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPGK•

Nucleotides

ATGGGTTGGTCTTGCATCATTCTCTTTCTCGTCGCTACCGCAACTGGTGTACACTCCCAAGTTCAACTTCAAGAATCA
GGCCCCGGACTCGTTAAACCCTCTCAAACTCTCTCTCTTACTTGCACTGTATCCGATTACTCTATTACTTCAGACTAC
GCTTGGAACTGGATCAGACAATTTCCCGGAAAAGGACTCGAATGGATGGGATATATCTCTTACTCTGGCTCAACCT
CTTACAACCCCTCTCTCAAATCTCGAATAACAATCTCACGCGATACTTCTAAAAATCAATTCTCACTTCAACTTAAC
TCCGTTACTGCCGCCGACACTGCCGTTTACTACTGTGCTTCCTTCGATTACGCCCACGCTATGGATTATTGGGGACA
AGGAACTACCGTCACTGTCAGCTCAGCCAGCACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGC
ACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT
CAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGG
TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGG
GGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG
GAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGG
ACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA
GAAGAGCCTCTCCCTGTCCCCGGGTAAATGA

Fig. 30

HeRX-1 Low Risk Heavy Chain Gamma-4
Amino Acids
MGWSCIILFLVATATGVHSDVQLQESGPGLVKPSQTLSLTCTVTDYSITSDYAWNWIRQFPGKKLEWMGYISYSGSTSYN
PSLKSRITISRDTSKNQFSLQLNSVTAADTATYYCASFDYAHAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKY
GPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Nucleotides
cDNA
ATGGGATGGAGTTGCATTATACTTTTCCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACTTCAAGAATC
TGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCT
CCTACAATCCTTCTCTGAAATCACGCATCACAATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA
CCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGT
GGACAAGAGAGTTGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCA
GTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGA
CGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAA
GCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAC
GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTG
ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC
TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCA
GGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCT
CTCCCTGTCTCTGGGTAAATGA

Genomic
ATGGGATGGAGTTGCATTATACTTTTCCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACTTCAAGAATC
TGGCCCAGGTCTCGTCAAACCTTCTCAAACTCTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAATTTCCTGGTAAAAAACTCGAATGGATGGGTTATATTTCTTACTCTGGCTCCACCT
CCTACAATCCTTCTCTGAAATCACGCATCACAATTTCCCGCGATACCTCTAAAAATCAATTTTCACTCCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA
CCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGT
GGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCT
GGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCT
GACCACCCCACTCATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCGGGCAGCCACAGGCTGGATGC
CCCTACCCCAGGCCCTGCGCATACAGGGGCAGGTGCTGCGCTCAGACCTGCCAAGAGCCATATCCGGGAGGACCCT
GCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTG
AGTAACTCCCAATCTTCTCTCTGCAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCAGG
CCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTG
ACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCC
AAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGG
TCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACA
GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGT
CTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGG
GCCACATGGACAGAGGTCAGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGG
GCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC
CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA
CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGG
TGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCT
CCCTGTCTCTGGGTAAATGA